

FIG. 1A

poly C tract

26695 TATATCCCCTTTAATCAAGCAAACTTCACTCTAGCCCCCCCCCGGAAAA
x
UA802 TATATCCTCTTTAATCAAGCAAACTTCACTCTAGCCCCCCCCCGG--GAAAA

line 1

imperfect TAA repeats

HP0094 stop ***

TAATAAGAATAATAATAAAGAGAGGAAGAAATATCAGTGCAAGCTTCTTTGATTTTATGC
x x
TAATAAATAATAATAAAGAGAGGAAGAAATACCAAGCGCAAGCTTCTTTGATTTTATGC

line 2

CGCTAAAAACAGCGTGTGTGTCATATAAGAAGAGGGGATTATGTGGGGATTGGCTGTCA
x
CGCTAAAAACAGCGTATTGTGTCATATAAGAAGAGGGGATTATGTGGGGATTGGCTGTCA

line 3

... start of HP0093

GCTTGGTATTGACTATCAAAAAGGGCGTTGAGTATATGGCAAGCGCGTGCCAAACAT
x
GCTTGGTATTGATTATCAAAAAGGGCGTTGAGTATATGGCAAGCGCGTGCCAAACAT
*** stop of - 1 frame

line 4

FIG. 1B

```

GC
A   U
A   U
C       U
G   C
U   U
G.U
A-U | 0 frame
C-G |
U-A | Stop
A-U
U   U
A-U
A-U
AG   AGC

```

pGEMB3

T7 → (26695 *fucT2*)

H | E

pGEMH2

T7 → (802 *fucT2*, truncated)

H |

pGEMI6

T7 → (802 *fucT2*)

H |

FIG. 3A

Applicant(s): Diane Taylor et al.

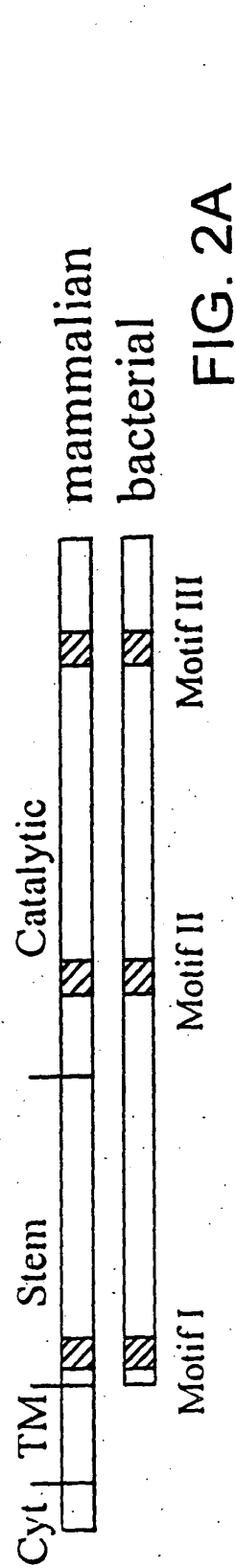
ALPHA 1,2 FUCOSYLTRANSFERASE

```

gaacactcac acgcgtcttt ttcaaataaa aaattcaaat gatttgaaag cggtacccca 60
cttttttaggc ttttattgaa aaagggcttt aaagttggct aaaacaggcg ttttatttga 120
aaaacaaagg gggtga atg gct ttt aaa gtg gtg caa att tgt ggg ggg ctt 172
Met Ala Phe Lys Val Val Gln Ile Cys Gly Gly Leu
      1           5           10
ggg aat caa atg ttt caa tac gct ttc gct aaa agt ttg caa aaa cac 220
Gly Asn Gln Met Phe Gln Tyr Ala Phe Ala Lys Ser Leu Gln Lys His
      15           20           25
ctt aat acg ccc gtg cta tta gac act act tct ttt gat tgg agc aat 268
Leu Asn Thr Pro Val Leu Leu Asp Thr Thr Ser Phe Asp Trp Ser Asn
      30           35           40
agg aaa atg caa tta gag ctt ttc cct att gat ttg ccc tat gcg aat 316
Arg Lys Met Gln Leu Glu Leu Phe Pro Ile Asp Leu Pro Tyr Ala Asn
      45           50           55           60
gca aaa gaa atc gct ata gct aaa atg caa cat ctc ccc aag tta gta 364
Ala Lys Glu Ile Ala Ile Ala Lys Met Gln His Leu Pro Lys Leu Val
      65           70           75
aga gat gca ctc aaa tac ata gga ttt gat agg gtg agt caa gaa atc 412
Arg Asp Ala Leu Lys Tyr Ile Gly Phe Asp Arg Val Ser Gln Glu Ile
      80           85           90
gtt ttt gaa tac gag cct aaa ttg tta aag cca agc cgt ttg act tat 460
Val Phe Glu Tyr Glu Pro Lys Leu Leu Lys Pro Ser Arg Leu Thr Tyr
      95           100           105
ttt ttt ggc tat ttc caa gat cca cga tat ttt gat gct ata tcc tct 508
Phe Phe Gly Tyr Phe Gln Asp Pro Arg Tyr Phe Asp Ala Ile Ser Ser
      110           115           120
tta atc aag caa acc ttc act cta ccc ccc ccc ccc gaa aat aat aaa 556
Leu Ile Lys Gln Thr Phe Thr Leu Pro Pro Pro Pro Glu Asn Asn Lys
      125           130           135           140
aat aat aat aaa aaa gag gaa gaa tac cag cgc aag ctt tct ttg att 604
Asn Asn Asn Lys Lys Glu Glu Glu Tyr Gln Arg Lys Leu Ser Leu Ile
      145           150           155
tta gcc gct aaa aac agc gta ttt gtg cat ata aga aga ggg gat tat 652
Leu Ala Ala Lys Asn Ser Val Phe Val His Ile Arg Arg Gly Asp Tyr
      160           165           170
gtg ggg att ggc tgt cag ctt ggt att gat tat caa aaa aag gcg ctt 700
Val Gly Ile Gly Cys Gln Leu Gly Ile Asp Tyr Gln Lys Lys Ala Leu
      175           180           185
gag tat atg gca aag cgc gtg cca aac atg gag ctt ttt gtg ttt tgc 748
Glu Tyr Met Ala Lys Arg Val Pro Asn Met Glu Leu Phe Val Phe Cys
      190           195           200
gaa gac tta aaa ttc acg caa aat ctt gat ctt ggc tac cct ttc acg 796
Glu Asp Leu Lys Phe Thr Gln Asn Leu Asp Leu Gly Tyr Pro Phe Thr
      205           210           215           220
gac atg acc act agg gat aaa gaa gaa gag gcg tat tgg gat atg ctg 844
Asp Met Thr Thr Arg Asp Lys Glu Glu Glu Ala Tyr Trp Asp Met Leu
      225           230           235
ctc atg caa tct tgc aag cat ggc att atc gct aat agc act tat agc 892
Leu Met Gln Ser Cys Lys His Gly Ile Ile Ala Asn Ser Thr Tyr Ser
      240           245           250
tgg tgg gcg gct tat ttg atg gaa aat cca gaa aaa atc att att ggc 940
Trp Trp Ala Ala Tyr Leu Met Glu Asn Pro Glu Lys Ile Ile Ile Gly
      255           260           265
ccc aaa cac tgg ctt ttt ggg cat gaa aat att ctt tgt aag gaa tgg 988
Pro Lys His Trp Leu Phe Gly His Glu Asn Ile Leu Cys Lys Glu Trp
      270           275           280
gtg aaa ata gaa tcc cat ttt gag gta aaa tcc caa aaa tat aac gct 1036
Val Lys Ile Glu Ser His Phe Glu Val Lys Ser Gln Lys Tyr Asn Ala
      285           290           295           300
taaaagcggct taaaaaaagg gcttactaga ggcttaatct ttgatttttag atcgatttc 1096
tttatagcga gcgtctaatt cta 1119

```

FIG. 1D



	Motif I	Motif II	Motif III
man Fut1 (365 aa)	GREGNQMGQYA (87-97)	VGHVRRRGDYL (215-225)	GTEGFWAAAYL (308-317)
man Fut2 (343 aa)	GRLGNQMGEYA (70-80)	VGHVRRRGDYL (196-206)	GTEGIWAAAYL (289-298)
Hp FutT2 (300 aa)	GGLGNQMFQYA (10-20)	VEVHIRRGDYL (163-173)	STYSWWAAAYL (249-258)
Ye WbcH (283 aa)	GGLGNQLFQVA (9-19)	VGIHIRRGDFV (158-168)	STFSWWAAAIL (241-250)
L1 EpsH (309 aa)	GNLGNQLFIYA (8-18)	ICVSIRRGDYL (173-183)	SSFSWWTEFL (263-272)

FIG. 2B

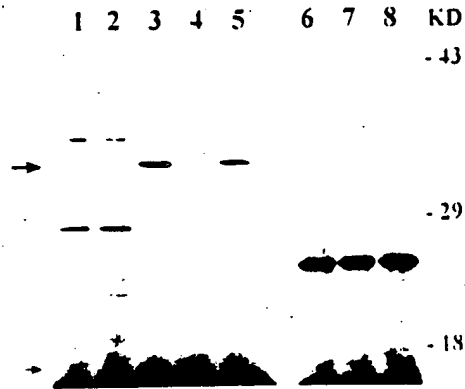


FIG. 3B

UA802 wt

ΔH

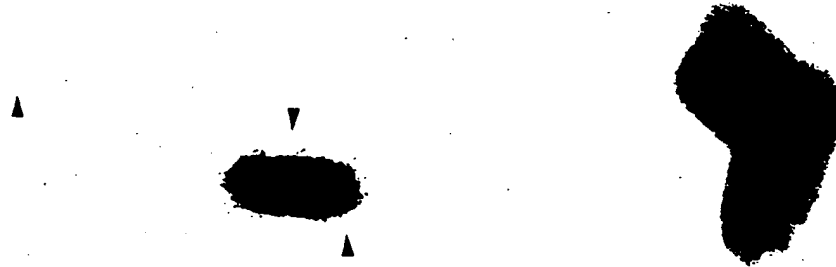


FIG. 4

26695 UA802
 WT ΔH ΔE WT ΔH ΔE

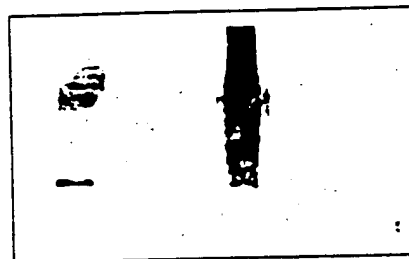


FIG. 6A

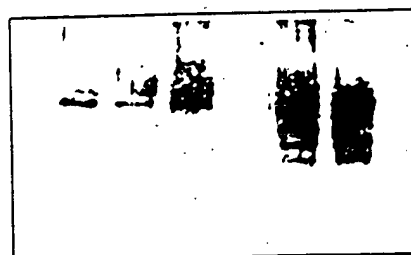


FIG. 6B

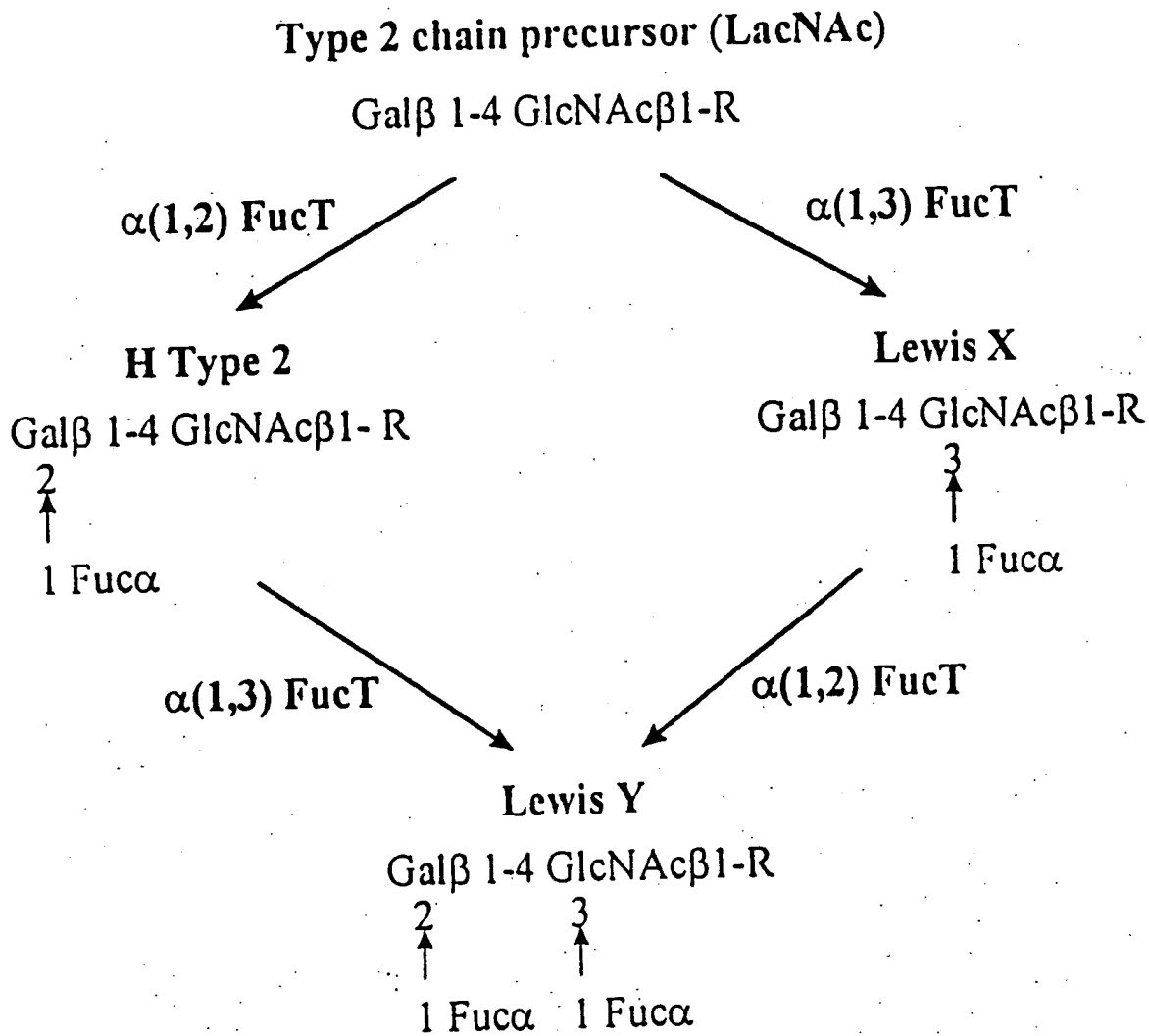


FIG. 5

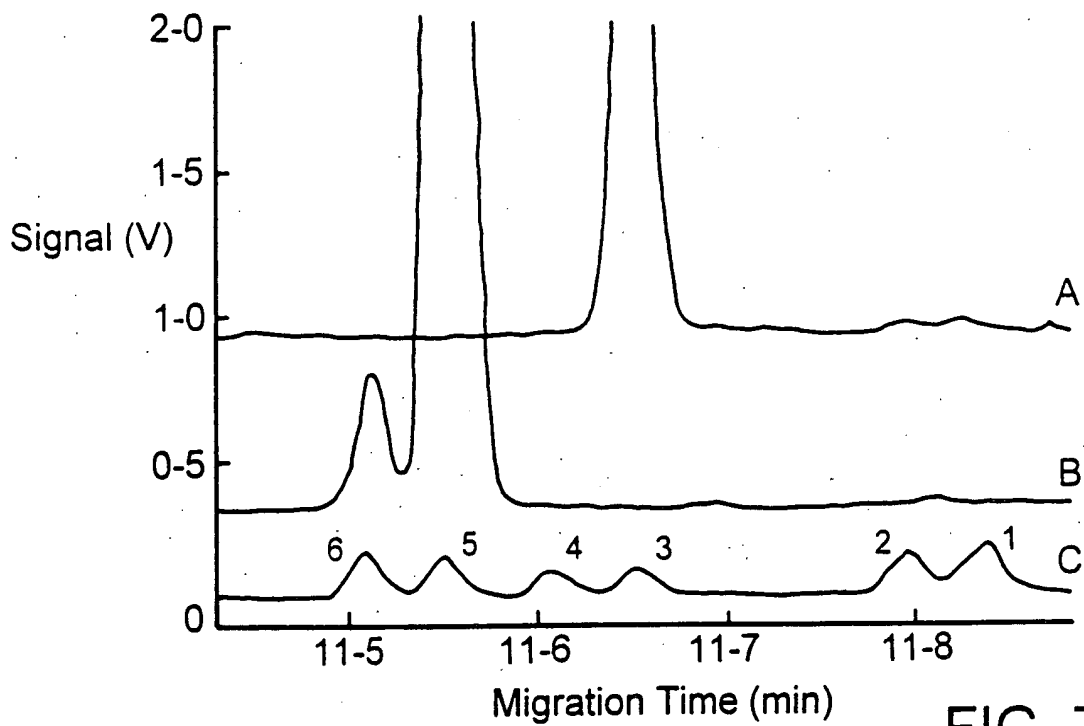


FIG. 7A

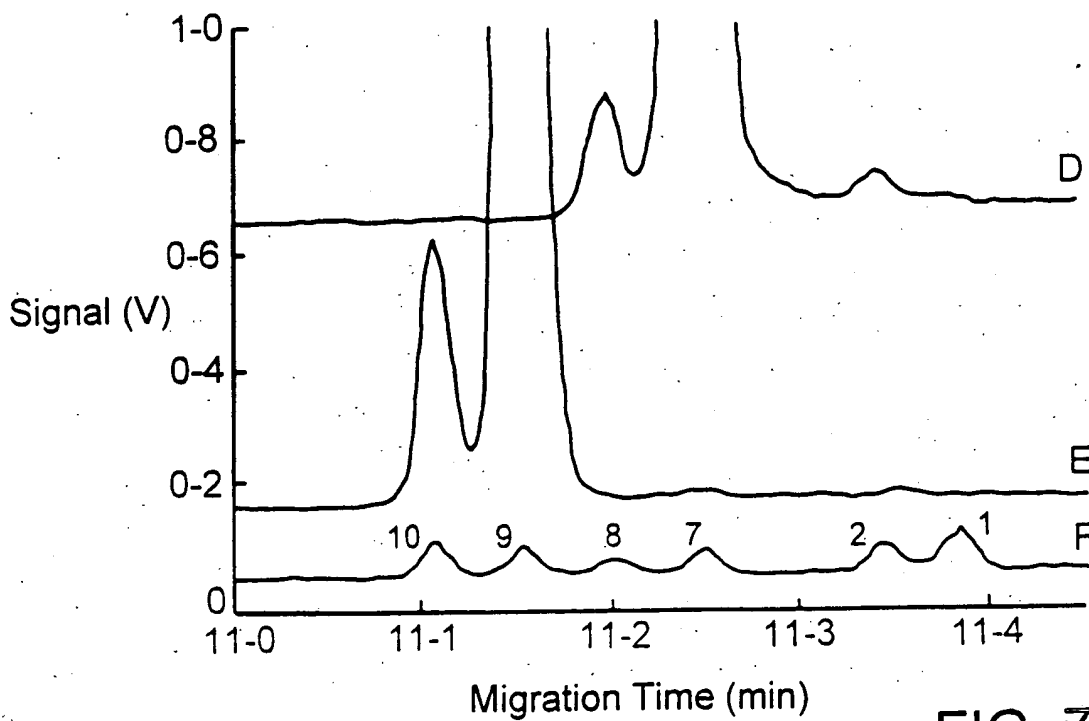


FIG. 7B

